RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/565,263_

Source: _IFWP_

Date Processed by STIC: _1-27-06_

ENTERED

RAW SEQUENCE LISTING   DATE: 01/27/2006
PATENT APPLICATION: US/10/565,263   TIME: 09:38:33

Input Set : **A:\ASZD-P01-136.txt**
Output Set: **N:\CRF4\01272006\J565263.raw**

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   3 <110> APPLICANT: Carlsson, Bjorn
   4         Olsson, Per Georg
   6 <120> TITLE OF INVENTION: GENETIC MARKER FOR CORONARY ARTERY DISEASE
   8 <130> FILE REFERENCE: ASZD-P01-136
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/565,263
C--> 10 <141> CURRENT FILING DATE: 2006-01-18
  10 <150> PRIOR APPLICATION NUMBER: SE 0302122-7
  11 <151> PRIOR FILING DATE: 2003-07-22
  13 <160> NUMBER OF SEQ ID NOS: 54
  15 <170> SOFTWARE: PatentIn version 3.2
  17 <210> SEQ ID NO: 1
  18 <211> LENGTH: 121
  19 <212> TYPE: DNA
  20 <213> ORGANISM: Homo sapiens
  22 <400> SEQUENCE: 1
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  25 rccacgtccc cggggtctca gtccctgggt caacgcagag aggctcgcgg tccgcggtgc     120
  27 t                                                                     121
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  31 <211> LENGTH: 121
  32 <212> TYPE: DNA
  33 <213> ORGANISM: Homo sapiens
  35 <400> SEQUENCE: 2
  36 ggaggcgacc ggggcgcctc tgctccggag ggggcagagg agggagggag cgccgggcac      60
  38 mgcgcccggt atctttctgc gcttgactgg ccgggaggaa gggggtgaca ctggggcacc     120
  40 c                                                                     121
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  44 <211> LENGTH: 121
  45 <212> TYPE: DNA
  46 <213> ORGANISM: Homo sapiens
  48 <400> SEQUENCE: 3
  49 cctcatccag acgctccgct agtgcagaca ggagcgcgca gtggccccgg ctcgccgcgc      60
  51 yatggagcgg atccccagcg cgcaaccacc ccccgcctgc ctgcccaaag caccgggact     120
  53 g                                                                     121
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  57 <211> LENGTH: 121
  58 <212> TYPE: DNA
  59 <213> ORGANISM: Homo sapiens
  62 <220> FEATURE:
  63 <221> NAME/KEY: misc_feature
  64 <222> LOCATION: (61)..(61)
  65 <223> OTHER INFORMATION: n is a, c, g, or t
  67 <400> SEQUENCE: 4
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      68 caggatgtac cctgcccaca tgtaccaagt gtacaagtca agacggggaa taaagcggag    60
W--> 70 ngaggacagc aaggtaagca agtgcacccc tagggaccct gcgctcagcc cctcgcgcgc   120
      72 g                                                                   121
      75 <210> SEQ ID NO: 5
      76 <211> LENGTH: 121
      77 <212> TYPE: DNA
      78 <213> ORGANISM: Homo sapiens
      80 <400> SEQUENCE: 5
      81 agacaggtgg cacccgtttt tttaaattat ttaattatat atatatatta tatatatata    60
      83 yacacacaca cacacacaca catatatgag tgtatctgtc tatcttttta aaagcatgac   120
      85 c                                                                   121
      88 <210> SEQ ID NO: 6
      89 <211> LENGTH: 105
      90 <212> TYPE: DNA
      91 <213> ORGANISM: Homo sapiens
      94 <220> FEATURE:
      95 <221> NAME/KEY: misc_feature
      96 <222> LOCATION: (61)..(62)
      97 <223> OTHER INFORMATION: AT is a repeat of 4-7 units;
      99 <220> FEATURE:
     100 <221> NAME/KEY: misc_feature
     101 <222> LOCATION: (63)..(64)
     102 <223> OTHER INFORMATION: AC is a repeat of 8-15 units;
     104 <400> SEQUENCE: 6
     105 aatgcctcca aagacaggtg gcacccgttt ttttaaatta tttaattata tatatatatt    60
     107 atacatatat gagtgtatct gtctatcttt ttaaaagcat cacct                   105
     110 <210> SEQ ID NO: 7
     111 <211> LENGTH: 121
     112 <212> TYPE: DNA
     113 <213> ORGANISM: Homo sapiens
     115 <400> SEQUENCE: 7
     116 atcagaccca gctcccaaag tgatggactt caaggaaaaa cccagctctc cggccaaagg    60
     118 ytcggaaggt cctgggaaaa actgcgtgcc agtcatccag cggactttcg ctcactcgag   120
     120 t                                                                   121
     123 <210> SEQ ID NO: 8
     124 <211> LENGTH: 121
     125 <212> TYPE: DNA
     126 <213> ORGANISM: Homo sapiens
     128 <400> SEQUENCE: 8
     129 actgcgtgcc agtcatccag cggactttcg ctcactcgag tggggagcag agcggcagcg    60
     131 rcacggacac agacagtggc tatggaggag aatcggagaa gggcgacttg cgcagtgagc   120
     133 a                                                                   121
     136 <210> SEQ ID NO: 9
     137 <211> LENGTH: 122
     138 <212> TYPE: DNA
     139 <213> ORGANISM: Homo sapiens
     142 <220> FEATURE:
     143 <221> NAME/KEY: misc_feature
     144 <222> LOCATION: (61)..(62)
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RAW SEQUENCE LISTING   DATE: 01/27/2006
PATENT APPLICATION: US/10/565,263   TIME: 09:38:33

            Input Set : A:\ASZD-P01-136.txt
            Output Set: N:\CRF4\01272006\J565263.raw

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145 <223> OTHER INFORMATION: AT is a repeat of 12-22 units;
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150 gtatgtgcgt gtgcgtgcac atgtgtgcct gcgtgttggt ataggacttt aaagctcctt     120
152 tt                                                                    122
155 <210> SEQ ID NO: 10
156 <211> LENGTH: 121
157 <212> TYPE: DNA
158 <213> ORGANISM: Homo sapiens
160 <400> SEQUENCE: 10
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163 sgggggattg tagcagacgt ctgggctttt ccccacccag agaatagccc ccttcgatac      120
165 a                                                                     121
168 <210> SEQ ID NO: 11
169 <211> LENGTH: 121
170 <212> TYPE: DNA
171 <213> ORGANISM: Homo sapiens
173 <400> SEQUENCE: 11
174 aagctccttt tggcataggg aagtcacgaa ggattgcttg acatcaggag acttgggggg       60
176 kattgtagca gacgtctggg cttttcccca cccagagaat agccccccttc gatacacatc     120
178 a                                                                     121
181 <210> SEQ ID NO: 12
182 <211> LENGTH: 121
183 <212> TYPE: DNA
184 <213> ORGANISM: Homo sapiens
186 <400> SEQUENCE: 12
187 tccttttggc atagggaagt cacgaaggat tgcttgacat caggagactt ggggggggatt      60
189 rtagcagacg tctgggcttt tccccacccca gagaatagcc cccttcgata cacatcagct     120
191 g                                                          121
194 <210> SEQ ID NO: 13
195 <211> LENGTH: 121
196 <212> TYPE: DNA
197 <213> ORGANISM: Homo sapiens
199 <400> SEQUENCE: 13
200 catagcacgg tagtggtttg gggaggtttc cgcaggtctg ctccccaccc ctgcctcgga       60
202 rgaataaaga gaatgtagtt ccctactcag gctttcgtag tgattagctt actaaggaac      120
204 t                                                                     121
207 <210> SEQ ID NO: 14
208 <211> LENGTH: 121
209 <212> TYPE: DNA
210 <213> ORGANISM: Homo sapiens
212 <400> SEQUENCE: 14
213 caacggcata tggagtgtcc ttattgctaa aaaggattcc gtctccttca aagaagtttt       60
215 wtttttggtc cagagtactt gttttcccga tgtgtccagc cagctccgca gcagcttttc      120
217 a                                                                     121
220 <210> SEQ ID NO: 15
221 <211> LENGTH: 121
222 <212> TYPE: DNA
223 <213> ORGANISM: Homo sapiens
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Input Set : A:\ASZD-P01-136.txt
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225 <400> SEQUENCE: 15
226 tatataaata tattaaaaag gaaaatgttt cagatgttta tttgtataat tacttgattc    60
228 mcacagtgag aaaaaatgaa tgtattcctg tttttgaaga gaagaataat ttttttttc    120
230 t                                                                    121
233 <210> SEQ ID NO: 16
234 <211> LENGTH: 121
235 <212> TYPE: DNA
236 <213> ORGANISM: Homo sapiens
238 <400> SEQUENCE: 16
239 tatttgtata attacttgat tcacacagtg agaaaaaatg aatgtattcc tgtttttgaa    60
241 ragaagaata attttttttt tctctaggga gaggtacagt gtttatattt tggagccttc .  120
243 c                                                                    121
246 <210> SEQ ID NO: 17
247 <211> LENGTH: 121
248 <212> TYPE: DNA
249 <213> ORGANISM: Homo sapiens
251 <400> SEQUENCE: 17
252 gaaggtgtaa aattgtaaat attttatct atgagtaaat gttaagtagt tgttttaaaa    60
254 wacttaataa aataattctt ttcctgtgga agagaaagat ggtctcctga gttttttaaa   120
256 a                                                                    121
259 <210> SEQ ID NO: 18
260 <211> LENGTH: 412
261 <212> TYPE: PRT
262 <213> ORGANISM: Homo sapiens
264 <400> SEQUENCE: 18
266 Met Glu Arg Ile Pro Ser Ala Gln Pro Pro Pro Ala Cys Leu Pro Lys
267 1               5                   10                  15
270 Ala Pro Gly Leu Glu His Gly Asp Leu Pro Gly Met Tyr Pro Ala His
271             20                  25                  30
274 Met Tyr Gln Val Tyr Lys Ser Arg Arg Gly Ile Lys Arg Ser Glu Asp
275         35                  40                  45
278 Ser Lys Glu Thr Tyr Lys Leu Pro His Arg Leu Ile Glu Lys Lys Arg
279     50                  55                  60
282 Arg Asp Arg Ile Asn Glu Cys Ile Ala Gln Leu Lys Asp Leu Leu Pro
283 65                  70                  75              .   80
286 Glu His Leu Lys Leu Thr Thr Leu Gly His Leu Glu Lys Ala Val Val
287             85                  90                  95
290 Leu Glu Leu Thr Leu Lys His Val Lys Ala Leu Thr Asn Leu Ile Asp`
291             100·                105                 110
294 Gln Gln Gln Gln Lys Ile Ile Ala Leu Gln Ser Gly Leu Gln Ala Gly
295         115                 120                 125
298 Glu Leu Ser Gly Arg Asn Val Glu Thr Gly Gln Glu Met Phe Cys Ser
299     130                 135                 140
302 Gly Phe Gln Thr Cys Ala Arg Glu Val Leu Gln Tyr Leu Ala Lys His
303 145                 150                 155                 160
306 Glu Asn Thr Arg Asp Leu Lys Ser Ser Gln Leu Val Thr His Leu His
307         ·       165                 170                 175
310 Arg Val Val Ser Glu Leu Leu Gln Gly Gly Thr Ser Arg Lys Pro Ser
311             180                 185                 190
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```
314 Asp Pro Ala Pro Lys Val Met Asp Phe Lys Glu Lys Pro Ser Ser Pro
315         195                 200                 205
318 Ala Lys Gly Ser Glu Gly Pro Gly Lys Asn Cys Val Pro Val Ile Gln
319         210                 215                 220
322 Arg Thr Phe Ala His Ser Ser Gly Glu Gln Ser Gly Ser Asp Thr Asp
323 225                 230                 235                 240
326 Thr Asp Ser Gly Tyr Gly Gly Glu Ser Glu Lys Gly Asp Leu Arg Ser
327                 245                 250                 255
330 Glu Gln Pro Cys Phe Lys Ser Asp His Gly Arg Arg Phe Thr Met Gly
331         260                 265                 270
334 Glu Arg Ile Gly Ala Ile Lys Gln Glu Ser Glu Glu Pro Pro Thr Lys
335         275                 280                 285
338 Lys Asn Arg Met Gln Leu Ser Asp Asp Glu Gly His Phe Thr Ser Ser
339         290                 295                 300
342 Asp Leu Ile Ser Ser Pro Phe Leu Gly Pro His Pro His Gln Pro Pro
343 305                 310                 315                 320
346 Phe Cys Leu Pro Phe Tyr Leu Ile Pro Pro Ser Ala Thr Ala Tyr Leu
347                 325                 330                 335
350 Pro Met Leu Glu Lys Cys Trp Tyr Pro Thr Ser Val Pro Val Leu Tyr
351         340                 345                 350
354 Pro Gly Leu Asn Ala Ser Ala Ala Ala Leu Ser Ser Phe Met Asn Pro
355         355                 360                 365
358 Asp Lys Ile Ser Ala Pro Leu Leu Met Pro Gln Arg Leu Pro Ser Pro
359         370                 375                 380
362 Leu Pro Ala His Pro Ser Val Asp Ser Ser Val Leu Leu Gln Ala Leu
363 385                 390                 395                 400
366 Lys Pro Ile Pro Pro Leu Asn Leu Glu Thr Lys Asp
367                 405                 410
370 <210> SEQ ID NO: 19
371 <211> LENGTH: 2922
372 <212> TYPE: DNA
373 <213> ORGANISM: Homo sapiens
375 <400> SEQUENCE: 19
376 ggacaccggg ccatgcacgc ccccaactga agctgcatct caaagccgaa gattccagca    60
378 gcccagggga tttcaaagag ctcagactca gaggaacatc tgcggagaga cccccgaagc   120
380 cctctccagg gcagtcctca tccagacgct ccgctagtgc agacaggagc gcgcagtggc   180
382 cccggctcgc cgcgccatgg agcggatccc cagcgcgcaa ccaccccccg cctgcctgcc   240
384 caaagcaccg ggactggagc acggagacct accagggatg taccctgccc acatgtacca   300
386 agtgtacaag tcaagacggg gaataaagcg gagcgaggac agcaaggaga cctacaaatt   360
388 gccgcaccgg ctcatcgaga aaaagagacg tgaccggatt aacgagtgca tcgcccagct   420
390 gaaggatctc ctacccgaac atctcaaact tacaactttg ggtcacttgg aaaaagcagt   480
392 ggttcttgaa cttaccttga agcatgtgaa agcactaaca aacctaattg atcagcagca   540
394 gcagaaaatc attgccctgc agagtggttt acaagctggt gagctgtcag ggagaaatgt   600
396 cgaaacaggt caagagatgt tctgctcagg tttccagaca tgtgcccggg aggtgcttca   660
398 gtatctggcc aagcacgaga cactcgggga cctgaagtct tcgcagcttg tcacccacct   720
400 ccaccgggtg gtctcggagc tgctgcaggg tggtacctcc aggaagccat cagacccagc   780
402 tcccaaagtg atggacttca aggaaaaacc cagctctccg gccaaaggtt cggaaggtcc   840
404 tgggaaaaac tgcgtgccag tcatccagcg gactttcgct cactcgagtg gggagcagag   900
406 cggcagcgac acggacacag acagtggcta tggaggagaa tcggagaagg gcgacttgcg   960
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 01/27/2006
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            Input Set : A:\ASZD-P01-136.txt
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<u>Please Note:</u>
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:4; N Pos. 61

VERIFICATION SUMMARY   DATE: 01/27/2006
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```
L:10 M:270 C: Current Application Number differs, Replaced Current Application No
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:70 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:60
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